Environmental Assessment and Planning of a Traunsboundary Fluvio-Marine Ecosystem: the Río de la Plata and its Maritime Front

CHAPTER 9. Fish Diversity of the Río de la Plata and its Maritime Front

FISHES FROM THE RÍO DE LA PLATA, THE ESTUARY AND ADJACENT SHELF AND SLOPE

Mirta L. García [1] Andrés J. Jaureguizar[2], Hugo L. López[1], Amalia M. Miquelarena[1], Roberto C. Menni[1], Lucila C. Protogino[3] and Graciela García[4]

[1] Museo de la Plata, Paseo del Bosque S/N. 1900. La Plata. Argentina.

[2] Instituto Nacional de Investigación y Desarrollo Pesquero

[3] Instituto de Limnología "Dr. Raúl Ringuelet"

FALTA 4

Email: mlgarcia@fcnym.unlp.edu.ar

ABSTRACT

The Río de La Plata has been traditionally divided in three zones, internal, intermediate and external, with clear geographic limits and distinctive environmental traits. The ichthyofauna is composed by freshwater, brackish and marine species which occurs along a longitudinal ecological gradient. Distribution of species throughout this gradient allows us to recognize two defined areas: a Riverine area characterized by a freshwater fish assemblage and an Estuarine area with an assemblage composed by freshwater, brackish water and marine fishes, including migrant species which use this space as nursery area. Following the gradient to the southwest we establish other two areas; one adjacent to the Río de la Plata (the Shelf area) and a following one (the Slope area), both with more

stable environmental and only marine fishes. Temperature and bottom salinity were identified as the determinant factors of these associations. Along the gradient, changes in the food energy source from benthic production or detritus to phytoplankton and zooplankton evidence their importance in structuring demersal fish communities. Analysis of population genetic structure analyses of commercial important fishes shows the existence of different genetic stocks which may be considered as management units in sustainable fisheries.

1. The fish fauna

It is somewhat peculiar that the fish taxonomy of the largest freshwater and brackish environment common to Argentina and Uruguay has not been really methodically studied. Probably the most important motive for this is its dimensions that except in coastal areas require large scale sampling methods. To this is added the lack of continuity and support to the creation of hydrobiological stations, in spite of proposal to that end since over a century (Popovici and Righi 1948). The best known part, which has been the subject of systematic research with oceanic methodologies, is the external zone (also marine section and/or estuarial zone). So, in lists of the Río de la Plata fishes, there are reported marine species which in fact strictly belong to brackish waters. The typical cases are lists that include only a few freshwater fishes (Marelli 1924, De Buen 1950, Cousseau 1985, Lasta 1995). Among the first fish reports for the Río de la Plata, are *Pimelodus maculatus* by Lacépède (1803), *Genidens barbus* by Quoy and Gaimard in 1824, and *Odontesthes bonariensis*, *Loricariichthys anus* and *Hypostomus commersoni* by Valenciennes in 1835 and 1836 (Ringuelet et al. 1967).

Detailed lists of the RÍo de la Plata freshwater fishes were only available with the publication of lists by López et al. (1996) and Nion (1998), though many adequate data may be obtained from the book by Ringuelet et al. (1967), where the Río de la Plata is included as a single locality among many others. Many other localities in the river are reported by Menni et al. (1984). Any analysis of the available lists will clearly show that the fish fauna from the Río de la Plata is typically Brazilian or Paranensean in the sense of Ringuelet et al. (1967) and Ringuelet (1975), and that is very similar to that from the Paraná River.

The Río de la Plata, together with the Paraná River and the lower section of the Paraguay River, conform the Subtropical Potamic Axis (López et al. 2002) or the Great Rivers Province (López et al. 2008). The Paraná River Delta, with a well known Paranensean abundant fish fauna (164 species) (Liotta et al. 1995/1996), is adequate for comparative purposes. Nion (1998) listed 153 species from the Río de la Plata, 9 less than the Delta and Menni (2004) lists 166. In this paper we listed 161 species (Table 1) Environments of the Province of Buenos Aires (Argentina), connected with the Río de la Plata (Almirón et al. 2000) have a number of fish species about 30% of that from the River, a similar relation to that found between the Paraná River and related environments.

Considering that these environments in the Province of Buenos Aires, largely poorer that the Río de la Plata, have given origin to a enormous amount of empirical and theoretical information (Ringuelet 1962, 1975, references in López et al. 2006), we may have an idea of the magnitude of investigation required for an adequate knowledge of the Río de la Plata.

From a taxonomic point of view, the fish composition of the Río de la Plata has been naturally influenced by the important nomenclatural changes raised in the last decades, especially in the Characiformes. These changes may be followed through the lists published in different moments (Marelli 1924, Pozzi 1945, Ringuelet and Arámburu 1957, Ringuelet et al. 1967, Almirón et al. 1992, López et al. 1996, Nión 1998, Menni 2004).

The low variation in number of families and species of Siluriformes (except in relation to the oldest lists), show that the knowledge of species of this group is more complete than that of the other orders. In this case, as in others, it is possible than smaller or rarer species has been yet overlooked. Species number of Gymnotifomes practically doubled between first and latest lists. In other orders changes were lesser.

The number of species occurring in the Río de la Plata is about 35% of the total number given for Argentina (López et al. 2003). Among exotic fish, the carp is the most important because the wide distribution the species reached in few more than a half century (McDonagh 1945), invading inner waters of the Buenos Aires Province and totally occupying the Salado River Basin (López et al. 1996). More recent introductions were *A.cf. baerii* and *H. molitrix* (Azpelicueta and Almirón 1999, García Romero et al. 1998).

Cousseau (1985) provides a list of fishes mainly from the maritime front, including some species from the river itself, based in De Buen (1950), Abella et al. (1979), Ringuelet et al. (1967) and research trips from the Instituto Nacional de Investigación y Desarrollo Pesquero. She mentions six freshwater species (four siluriforms and two chaciforms). García et al. (2003) report 19 chondrichthyan species (all marine ones with the exception of *P. brachyura*), 170 freshwater species and 73 marine species.

To the West of the external zone there is large environment, the Samborombón Bay with a dense net of tide influenced environments which give to the bay physical, chemical and environmental traits that provides the basic conditions for the establishment of juveniles (Lasta 1995).

The Samborombón Bay includes retention, high productivity and nursering zones (Acha and Mianzan 2003). Lasta (1995) reports for bay five freshwater species (four siluriforms and a single caraciform). These numbers show that the ichthyofauna from the area is a combination of freshwater, brackish and marine species. The northern and southern areas of the bay show minimum values of specific richness, diversity and equitability. Six and a half percent of the species (*M. furnieri,* and *M. ancylodon*) are **permanent** ones (*i.e*. presence >75%); 48,4% are **frequent** species (between 10% and 50% of species, *B. aurea*, *A. marini, M. platanus*, *Odontesthes* sp., *P. brasiliensis, P. signata, P. cromis, P. valencienessi, flatfishes, M. americanus, S. brasilensis, C. striatus*, *M. goodei*, *C. carpio* and *L. grossidens*), and el 43.1% are **occasional species** (presence <10%, *P. nudigula*, *P. saltatrix*, *U. canosai*, *Astyanax* spp, *Corydoras* sp., *Acanthistius brasilianus*, *Engraulis anchoita, G. barbus*, *P. pororosissimus*, *S. plagiusa*, *Ramnogaster arcuata*, *P. albicans* and *P. maculatus*). Marine species (*P. signata* and flounders of the genera *Paralichthys* and *Xystreurys*) and some freshwater species (*P.valencienessi* and *C. carpio*) co-exist within a salinity range from 12 to 14 SPU. When salinity values are higher or lower, there are present only strictly marine or freshwater species respectively (Lasta 1995).

The seasonal variation in the specific composition within Samborombón Bay appears related to the spatial extension of the fish assemblages of the estuary which depends of the bi-modal discharge pattern of the Río de la Plata (Jaureguizar et al 2003, 2004, 2006). There also changes due to seasonal migrations.

Brevoortia aurea and *P. cromis* spawn in the bay (Lasta 1995, Macchi et al. 2002), which is the main reproductive area of resident species as *B. aurea* and *M. ancylodon* and migratory ones as *M. furnieri* and *Mugil* sp. *A. marinii* and *Odontesthes sp*. (8.8% of the species) developed all their life cycles within the Bay. Other, as *M. furnieri, M. ancylodon* and *M. platanus*, have in the Bay zones of larvae and breeding concentration. There is a large percentage of species (*P. brasiliensis*, *G. barbus*, *P. signata*, flatfish, *M. americanus*, *P. cromis*, *U. brasiliensis, C. orbignyanus*, *P.valencienessi*, *S. plagiusa*, *P. albicans* and *P. maculatus*), that appear as juvenile and adult but do not reproduce in the Bay (Lasta 1995).

2. Fish assemblages from Río de la Plata and its Martime Front

2.1. Fish assemblages from the river to the slope

The Río de la Plata and its Marine Front ichthyofauna has a strong spatial arrangement along the environment gradient from the fresh and shallow water (3.5 m) to marine deeper water (323.5 m). The species composition, defines four main areas: riverine, estuarine, shelf and slope (Fig. 1). These areas, consistently distinguishable by their environmental conditions (Table 2) and consistent boundaries, evidence a gradual change from riverine to marine communities rather than a distinct single transition (Fig. 2) (García et al. 2010).

The riverine area covers the inner part of the Río de la Plata and is characterized by fresh water, shallow depth and the highest water temperature (Fig. 1, Table 2). The fish composition has the highest similarity, and is mainly dominated by freshwater species (*P. vetula*, *P. albicans, L. obtusidens, P. granulosus, C. carpio,* and *L. pati*), and anadromous species (G. barbus and *L. grossidens*) (Fig. 2). The anadromous species, G. barbus during spring and early summer and *L. grossidens* during the autumn and early winter, penetrates into the Río de la Plata and rivers from the Río de la Plata basin to spawn (Fuster de Plaza and Boschi 1961, Ringuelet et al. 1967, Ringuelet 1975, Jaureguizar et al. 2003, Menni 2004).

In the Estuarine area (Fig. 1), with intermediate salinities and temperatures (Table 2), the fish community has an intermediate internal similarity associated to predominance of estuarine resident species (*M. furnieri, A. marinii, B. aurea, P. brasiliensis,* and *M. ancylodon),* and to a lower degree to occasional freshwater species (*P. albicans, P. valenciennis,* and *L. pati*) and marine species, either straggler (*C. guatucupa, C. orbignyanus* and *P. patagonicus*) or migrant (*P. punctatus* and *S. bonapartii*) (Fig. 2). The estuarine resident species use Samborombón Bay as the main nursery area (Lasta 1995). The straggler species (*C. guatucupa* and *P. patagonicus*) occurred more frequently in shelf waters, and carried on reproductive activity in coastal zones with salinity over 28 psu (Macchi and Acha 1998).

The area adjacent to the Río de la Plata (salty, intermediate depth and cool) form the shelf area (Fig. 1, Table 2), where the ichthyofauna has an intermediate internal similarity, and is mainly dominated by marine species, namely *T. lathami, M. schmitti, S. guggenheim, P. brasiliensis, P. nudigula, S.brasiliensis, M. argentinae, P. pagrus, M. furnieri* and *D. tschudii*.

The slope area covers the zone with the greatest depths, highest salinities, and the lowest temperatures (Fig. 1, Table 2) and its fish community showed the lowest internal similarity. In contrast with the shelf area, the slope assemblage is dominated by marine species associated with deep water (*S. acanthias*, *M. hubbsi, M. magellanicus, H. lahillei* and *B. albescens*) (Fig. 2).

This fish assemblage pattern is mainly influenced by the bottom salinity and temperature, and each area shows consistent boundaries which occur near the location of frontal zone (García et al. 2010) (Fig. 2). The riverine–estuarine border occurs where the halocline intersects the bottom, and corresponds to the bottom salinity front defined by Guerrero et al. (1997a, b). This represents a frontier for intrusions of freshwater species into the estuary (*L. pati, P. valenciennis, L. obtusidens, P. lineatus* and species of Loricariidae) (Boschi 1988, Jaureguizar et al. 2003). The border zone between the estuarine and shelf areas coincides with the location of the maximum horizontal gradient of surface salinity (Guerrero et al. 1997a, b), indicating the boundary between the estuary and the continental coastal waters (Mianzan et al. 2001). The persistent salinity vertical structure (Guerrero et al. 1997a, b) in the estuarine area (Fig. 2), shows the presence of a shelf water intrusion along the bottom, which allows the incursion of marine species toward the head of the estuary (Jaureguizar et al. 2003). This zone is the limit for the presence in the estuary of marine species as *M. argentinus, P. pagrus, M. hubbsi* and *T. lathami.* (Boschi 1988, Jaureguizar et al. 2003). The shelf-break front is near the border between shelf and slope fish assemblages. This front is a permanent feature that characterized the border of the shelf, and its inner boundary lies between 90 and 100 m isobaths (Acha et al. 2004). Here the sub Antarctic waters meet the cooler and more saline water of the Malvinas current, thus producing a thermohaline front (Lutz and Carreto 1991, Martos and Piccolo 1988).

The BIO-ENV process analysis identified surface and bottom salinity (ρ = 0.848, and ρ = 0.819 respectively) as the factors having the greatest influence on the fish assemblages distribution based on biomass. Bottom temperature (ρ = 0.828) was the next most influential factor on the fish assemblages distribution based on abundance. For both analyses the combination of temperature and bottom salinity present the best correlation coefficient (ρ = 0.906 and 0.917 respectively).

2.2. Fish assemblage composition in relation to feeding

Considering the species feeding, the fish assemblage composition reflects a transition from a fish community influenced by muddy deposits originated in the river, dominated by bottom or detritus feeders, to a fish community where the presence of marine pelagic or semi pelagic species becomes more important, where probably energy flow originating from bottom deposits is less important. In the second case, species feeding on small pelagic fish or crustaceans indicate that the energy derived from the phytoplankton and zooplankton production becomes more important. Most of the freshwater species are bottom or bottom related species, omnivorous and euriphagic (Ringuelet 1975, Menni 2004). *Pterodoras granulosus* (Panattieri and del Barco 1982, Darrigran and Colautti 1994, Ferriz et al. 2000) and *L. obtusidens* (Mastrarrigo 1950, Ringuelet et al. 1967) and have a similar diet. Due to their euriphagy, all these species have changed their diet because of the invasion of the Río de la Plata basin by the south eastern Asia molluscs *Corbicula fluminea* and *Limnoperna fortunei*, (Ferriz et al. 2000, García and Protogino 2005, García and Moltalto 2006). Genidens barbus is a benthophagous species. Juveniles of *L. grossidens* are planktophagous and adults are ichthyophagous (Ringuelet et al. 1967). Most of species in the estuarine area have benthic habits and feed on molluscs and crustaceans. *M. furnieri* adults mainly prey upon *Mactra isabelleana* and secondarily upon shrimps, cephalopods and polychaetes (Sánchez et al. 1991). Only *B. aurea* is planktophagous, preying on diatoms, dinoflagellates, and copepods (Sánchez 1999), but detritus has also been observed in its diet (Giangiobbe and Sánchez, 1993). In the shelf and slope, the feeding habits show a transition from a benthic diet, basically composed by molluscs, crustaceans and small fish, to a more bentho-pelagic diet composed by small pelagic fish and deep water crustaceans and occasionally zooplankton. Among fishes of these communities, *S. acanthias* prefers to prey on pelagic communities. The main food items are ctenophores, teleost fishes (*M. hubbsi, S. brasiliensis*, *E. anchoita, N. bergi,* notothenids and mictophids and cephalopods, and occasionally, epibenthic macrocrustaceans (Menni, 1985; García de la Rosa and Sánchez, 1997). *Mustelus schmitti* feed on crustaceans, polychaetes and fishes (Olivier et al. 1968, Menni, 1985). The principal dietary component of *S. guggenheim* ares bony fish, followed by crustaceans, shrimps, molluscs and polychaetes. The bony fish are mainly pelagic fishes such as *E. anchoita*, followed by demersal fishes such as *C. guatucupa* and *P. ramsayi*, *N. longipes* and *M. hubssi* (Cousseau 1973, Vögler et al. 2003). *Helicolenus lahillei* feeds on benthic and pelagic species, such as ctenophores, salps, crustaceans, squids and fishes (Cousseau and Perrotta 2000). Adult *M. hubbsi* mainly feed on pelagic and demersal-pelagic species, with the more common prey being zooplanctonics crustaceans amphipods and euphausids, cephalopods, fishes, and epibenthic microcrustaceans (Angelescu et al. 1958, Angelescu and Cousseau 1969, Angelescu and Prenski 1987, Ruiz and Fondacaro 1997, Cordo 1981, Sánchez and García de la Rosa 1999). Juveniles mainly prey on zooplankton and secondarily on cephalopods and epibenthic macrocrustaceans. *Trachurus lathami* feed on copepods and chaetognaths (Cousseau 1967). *Percophis brasiliensis* feed on fishes and squids (San Román 1972). *Macruronus magellanicus* is an eurybatic species, able to adapt to different depths and hydrological conditions. It feeds upon pelagic crustaceans, amphipods, cephalopods and small fishes like sardines and nototthenids (Angelescu and Gneri 1961, Bezzi 1984, Sánchez and Prenski 1996, Sánchez 1999).

Besides the important role played by salinity and temperature in habitat differentiation, the change in the food energy source from benthic production or detritus to phytoplankton and zooplankton evidence their importance in structuring demersal fish communities.

3. Assessing the genetic structure of fish populations

The genetic population structure of a fish species within a particular geographic area may take different forms. In fisheries biology the stock, rather than the local population, is frequently referred to as the basic unit for harvest and management. The stock concept should be redefined to be synonymous of a grouping that relates to reproductive relationships and has a genetic meaning (such as local population or genetic patch). Biologically sustainable management based on knowledge of this structure may reduce the risk for depletion of genetic resources (Laikre et al. 2005).

Up to date, most empirical population genetic studies have been based on genetic markers assumed to primarily reflect selectively neutral DNA variation (most allozymes, microsatellites and mtDNA markers). Recent molecular technique developments provide increased opportunities for studying markers known to be located within functional genes of potential importance for fitness (Cano et al. 2008).

3.1. Recent studies in population genetic structure in different ecotypes of fish of the Río de la Plata and its Maritime Front

3.1.1. Pelagic fish

Despite the lack of genetic differentiation on a large geographic scale, many studies on pelagic fish detected small but statistically significant genetic differentiation among samples collected from very proximate localities within a short interval of time (Grande 1985).

Brevoortia aurea. This is a migratory pelagic marine fish from the Southwestern Atlantic and an abundant commercial fish in the Río de la Plata and its Maritime Front. The Brazilian menhaden represents an important species model to investigate patterns of genetic differentiation. Based on *cyt-b* phylogeographic approach, García et al. (2008) showed unexpected high genetic structuring in this pelagic marine fish. The analyses suggested the existence of a long-term stability of the *B. aurea* schools, leading to a microgeographical genetic differentiation after the mixture of different stocks in the Río de la Plata and in the Atlantic Ocean from the associated estuarine environments. The data revealed that the recruitment of unrelated mtDNA haplotypes carried out by individuals within schools could be occurring in the same nursery areas, revealing the existence of many different maternal lineages. The AMOVA analysis revealed a high level of intrapopulation diversity consistent with an extensive and low regional structured population in *B. aurea*. The highest within-population estimates of gene diversity (Fig. 3, Table 3. a) found in the *cyt-b* data set of *B. aurea* could be also congruent with a scenario of a metapopulation, where floods generated by the opening of the sand bars in rivers and lagoons mix individuals across large distances.

Engraulis anchoita. The anchovy is widely distributed in tropical and sub-tropical waters of the southwestern Atlantic and spawn in open coastal areas in the inner continental shelf. Adults move during seasons between open coastal areas and bays, where they form large aggregations targeted by important fisheries (Araújo et al. 2008).

Present phylogeographic analysis based on cytochrome b sequences in *E. anchoita* from four different collecting regions (Fig. 3) revealed unexpected large values for haplotype diversity and nucleotide diversity (Table 3b). Phylogenetic reconstruction using neighbour joining tree based on HKY85 model of molecular substitution (Fig. 3) showed two major clusters of taxa. One major group included most and diverse haplotypes belonging to the inner continental shelf (at 35ºS-53ºW). The other one was integrated by haplotypes from the outer Río de la Plata, outer shelf and inner shelf (at 36ºS-54ºW). In the AMOVA analysis two grouping of samples hypothesis (outer Río de la Plata and inner shelf at 36ºS-54ºW vs. Outer shelf and inner continental shelf at 35ºS-53ºW) have obtained the largest percentage of molecular variance. This grouping hypothesis showed significant values of the among groups component (Φ_{CT}) of the molecular variance. These results agree with the presence of at less two different long-term genetic stocks of *E. anchoita* in the Río de la Plata and its Maritime Front. *E. anchoita* moves around southern Uruguay and northeastern Argentina from offshore toward the end of the year and northward in March to June (Csirke 2005). Differences among growth rates of anchovy larvae from Brazilian Southeastern Bight suggest that this taxon may conforms a distinct population from more southerly stocks (Castello and Castello 2003). Therefore the mix of different stocks in the border of the Río de la Plata estuary and Southwestern Atlantic Ocean may explain the high level of genetic diversity detected in *E. anchoita.*

3.1.2. Benthic fish

Squatina guggenheim. This is a benthic elasmobranchs that inhabits shelf and upper slope environments in temperate and tropical regions of the world (Compagno 1984). This species is one of the main coastal fishing resources having a wide geographic distribution from Espíritu Santo (Brazil) to central Patagonia, Argentina (Vooren and da Silva 1991), in waters 10–80 m deep (Cousseau and Figueroa 2001). Like other benthic elasmobranchs, it tends to have low dispersal capability, which usually results in specimens from nearby areas having almost no mixing. As this restricted mixing may produce different life history parameters, it is important to study possible life history differences within angel shark species, even at small geographic scales (Colonello et al. 2007).

Phylogeographic approach based on cytochrome b sequences in *S. guggenheim* from three different collecting regions revealed very low values of haplotype and nucleotide diversity (Table 3c). The phylogenetic reconstruction by using neighbour joining method based on GTR model of molecular substitution (Fig. 4) shows three major cluster. One well supported group integrated by haplotypes from the outer Río de la Plata and outer shelf, a second one conformed by samples from Atlantic Ocean coast and outer Río de la Plata, and the last one integrated only by different Atlantic Ocean coast haplotypes. Remarkably the most frequent haplotype 1 was shared by samples from the three aforementioned regions. Different grouping hypotheses performed in the AMOVA analysis failed to detect significant values in the geographic partition of the molecular variance (García et al. 2009). Though a high population structuring was expected, all present data support the hypothesis that *S. guggenheim* constitutes a single panmictic unit or genetic stock in the Río de la Plata and its Maritime Front.

3.1.3 Demersal fish

Micropogonias furnieri. Populations of this species are distributed from the southern Caribbean to the Gulf of San Matías in Argentina. The white croaker is an important commercial fishing resource and at present it is considered to be fully exploited. A population genetic analysis based on mitochondrial D-loop region (CR) (Pereira et al. 2009) detected the presence of two stocks of *M. furnieri* in three different areas (Bahía Blanca, Río de la Plata and Atlantic Ocean). Río de la Plata locality have the lower values of haplotype and nucleotide diversity as well as demographic signatures of population declination whereas Atlantic Ocean collecting sites showed the highest values of genetic diversity and signatures of a past recent population expansion.

3.2. Units for fishery management, conservation and potential effects of ignoring the structure.

Present population genetic data indicate a long-term stocks differentiation between Río de la Plata and the Atlantic Ocean environments since the Pleistocene both in *B. aurea* (García et al. 2008) and *M. furnieri* (Pereira et al. 2009). In *B. aurea* the analysis suggests that the metapopulation represents the management unit, as well as the need of the inclusion of the associated rivers and coastal lagoons which are responsible for the origin of the major genetic diversity, in a high priority conservation program within a Marine Protected Area System in the Southwestern Atlantic Ocean (García et al. 2008). Biologically improper management may result in overharvest of particular populations or population segments, resulting in extinction or reduction of genetic diversity within populations. In this sense the smallest population sizes and the lowest levels of genetic variability in *M. furnieri* from the Río de la Plata, make this stock vulnerable to over-exploitation (Pereira et al. 2009).

Though Csirke (2005) have suggest that *E. anchoita* could support a higher fishing pressure, present analyses claims for a stocks management as mechanism to retain the basal level of genetic diversity in this taxon.

Low level of population structure was evident in *S. guggenheim*. The lowest genetic diversity values detected in this taxon could be indicating the existence of a long-term population declination or a past recent population bottleneck making it highly vulnerable to overexploitation (García et al. 2009).

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Table 1. Fish species from the Río de la Plata and its Maritime Front. FS: freshwater species, BS: brackish species, MS: marine species.

	FS	BS	MS
Clase Chondrichthyes			
Familia Odontaspididae			
Carcharias taurus			X
Familia Lamnidae			
Alopias vulpinus			X
Familia Scyliorhinidae			
Schoederichthys bivius			X
Familia Carcharhinidae			
Carcharinus plumbeus			X
Familia Triakidae			
Galeorhinus galeus			X
Mustelus canis			X
Mustelus fasciatus			X
Mustelus schmitti			X
Familia Hexanchidae			
Hexanchus griseus			X
Notorhynchus cepedianus			X
Familia Shyrnidae			
Sphyrna zygaena			
Familia Squalidae			X
Squalus acanthias			
Squalus megalops			X
Squalus mitsukuri			X
Familia Squatinidae			X
Squatina argentina			
Squatina guggenheim			X
Familia Torpedinidae			X
Discopyge tschudii			
Familia Rhinobatidae			X
Rhinobatos horkelii			
Zapteyx brevirostris			X
Familia Rajidae			X
Atlantoraja castelnaui			
Atlantoraja cyclophora			X
Atlantoraja platana			X
Rioraja agasizi			X
Psamombatis bergi			X
Psammobatis rudis			X
Sympterygia acuta			
Sympterygia bonapartii			X
Zearaja flavirostris			X
Familia Dasyatidae			X
Dasyatis pastinaca			
Familia Potamotrygonidae			X
Potamotrygon brachyura			
Potamotrygon hystrix	X		
Potamotrygon motoro	X		
Familia Gymnuridae	X		
Gymnura altavela			
Familia Myliobatidae			X
Myliobatis freminvillii			X
Myliobatis goodei			X
Familia Callorhinchidae			
Callorhinchus callorhynchus			X
Clase Actinopterygii			
Familia Acipenseridae			
Acipenser cf. *baerii*	X	X	
Familia Congridae			
Conger orbignyanus		X	
Pseudoxenomystax albescens			X
Familia Pristigasteridae			X
Pellona flavipinnis	X		
Familia Engarulidae			
Anchoa marinii		X	
Engraulis anchoita			X
Lycengarulis grossidens		X	X
Familia Clupeidae			
Brevoortia aurea		X	
Platanichthys platana	X	X	
Ramnogaster arcuata,		X	
Ramnogaster melanostoma	X		
Familia Cyprinidae			
Cyprinus carpio	X	X	
Hypophthalmichthys molitrix	X		
Familia Parodontidae			
Apareiodon affinis	X		
Parodon nasus	X		
Familia Curimatidae			
Cyphocharax platanus	X		
Cyphocharax saladensis	X		
Cyphocharax spilotus	X		
Cyphocharax voga	X		
Potamorhina squamoralevis	X		
Steindachnerina biornata	X		
Steindachnerina brevipinna	X		
Familia Prochilodontidae			
Prochilodus lineatus	X		
Familia Anostomidae			
Abramites hypselonotus	X		
Leporinus acutidens	X		
Leporinus obtusidens	X		
Leporinus striatus	X		
Pseudanos trimaculatus	X		
Schizodon platae	X		
Pseudanos trimaculatus	X		
Schizodon platae	X		
Familia Crenuchidae			
Characidium rachovii	X		
Familia Gasteropelecidae			
Thoracocharax stellatus	X		
Familia Characidae			
Aphyocharax anisitsi	X		

Aphyocharax dentatus	X
Brycon orbygnianus	X
Charax stenopterus	X
Cynopotamus argenteus	X
Galeocharax humeralis	X
Roeboides affinis	X
Roeboides microlepis	X
Cheirodon interruptus	X
Heterocheirodon yatai	X
Serrapinnus calliurus	X
Diapoma terofali	X
Pseudocorynopoma doriai	X
Metynnis otuquensis	X
Mylossoma duriventre	X
Piaractus mesopotamicus	X
Pygocentrus nattereri	X
Serrasalmus marginatus	X
Serrasalmus maculatus	X
Poptella paraguayensis	X
Tetragonopterus argenteus	X
Triportheus nematurus	X
Incertae sedis	
Astyanax abramis	X
Astyanax asuncionensis	X
Astyanax eigenmanniorum	X
Astyanax erythropterus	X
Astyanax fasciatus	X
Bryconamericus iheringii	X
Bryconamericus stramineus	X
Ctenobrycon alleni	X
Hyphessobrycon anisitsi	X
Hyphessobrycon luetkenii	X
Hyphessobrycon meridionalis	X
Markiana nigripinnis	X
Oligosarcus hepsetus	X
Oligosarcus jenynsii	X
Oligosarcus oligolepis	X
Salminus brasiliensis	X
Familia Acestrorhynchidae	
Acestrorhynchus pantaneiro	X
Familia Cynodontidae	
Raphiodon vulpinus	X
Familia Erythrinidae	
Hoplias malabaricus	X
Familia Lebiasinidae	
Pyrrhulina australis	X
Familia Aspredinidae	
Bunocephalus doriae	X
Bunocephalus iheringii	X
Familia Trichomycteridae	
Scleronema angustirostre	X
Parastegophilus maculatus	X
Familia Callichthyidae	
Callichthys callichthys	X
Corydoras aeneus	X
Corydoras paleatus	X
Corydoras undulatus	X
Hoplosternum littorale	X
Familia Loricariidae	
Hisonotus maculipinnis	X
Macrotocinclus flexilis	X
Otocinclus vittatus	X
Brochiloricaria chauliodon	X
Farlowella hahni	X
Loricaria apeltogaster	X
Loricariichthys anus	X
Loricariichthys platymetopon	X
Paraloricaria commersonoides	X
Paraloricaria vetula	X
Ricola macrops	X
Rineloricaria felipponei	X
Rineloricaria lima	X
Rineloricaria pareiacantha	X
Rineloricaria thrissoceps	X
Sturisoma robustum	X
Hypostomus commersoni	X
Hypostomus laplatae	X
Hypostomus microstomus	X
Hypostomus punctatus	X
Rhinelepis strigosa	X
Ancistrus cirrhosus	X
Familia Pseudopimelodidae	
Mycroglanis cottoides	X
Familia Heptapteridae	
Heptapterus mustelinus	X
Pimelodella gracilis	X
Pimelodella laticeps	X
Rhamdia quelen	X
Familia Pimelodidae	
Bergiaria platana	X
Hemisorubim platyrhynchus	X
Hypophthalmus edentatus	X
Iheringichthys labrosus	X
Luciopimelodus argentinus	X
Luciopimelodus pati	X
Megalonema platanun	X
Parapimelodus valenciennis	X
Pimelodus albicans	X
Pimelodus argenteus	X
Pimelodus brevis	X
Pimelodus maculatus	X
Paulicea luetkeni	X
Pseudoplatystoma coruscans	X
Pseudoplatystoma reticulatum	X
Sorubim lima	X
Zungaro jahu	X
Familia Doradidae	

Oxydoras kneri			
Pterodoras granulosus	X		
Rhinodoras dorbignyi	X		
Familia Auchenipteridae			
Ageneiosus inermis	X		
Ageneiosus militaris	X		
Auchenipterus nigripinnis	X		
Auchenipterus osteomystax	X		
Trachelyopterus albicrux	X		
Trachelypterus striatulus	X		
Familia Ariidae			
Genidens barbus	X		
Familia Gymnotidae			
Gymnotus inaequilabiatus	X		
Familia Sternopygidae			
Eigenmannia trilineata	X		
Eigenmannia virescens	X		
Familia Rhamphichthyidae			
Rhamphichthys rostratus	X		
Familia Hypopomidae			
Hypopomus artedi	X		
Familia Apteronotidae			
Apteronotus albifrons	X		
Familia Macrouridae			
Coelorhynchus marinii			X
Familia Merlucciidae			
Macruronus magellanicus			X
Merluccius hubbsi			X
Familia Phycidae			
Urophycis brasiliensis		X	X
Familia Ophidiidae			
Genypterus blacodes			X
Raneya fluminensis			X
Familia Batrachoididae			
Porichthys porosissimus			X
Thalassophryne montevidensis			X
Triathalassothia argentina			X
Familia Mugilidae			
Mugil platanus	X	X	X
Familia Atherinopsidae			
Odontesthes argentinensis		X	X
Odontesthes bonariensis	X	X	
Odontesthes perugiae	X		
Odontesthes humensis	X		
Odontesthes retropinnis	X		
Familia Rivulidae			
Austrolebias bellotti	X		
Austrolebias elongates	X		
Austrolebias nigripinnis	X		
Familia Anablepidae			
Jenynsia multidentata	X	X	
Familia Poeciliidae			
Cnesterodon decemmaculatus	X	X	
Phalloceros caudimaculatus	X		
Phalloptychus januarius	X		
Poecilia vivipara	X		
Familia Zeidae			
Zenopsis conchifer			X
Familia Syngnatidae			
Hippocampus punctulatus			X
Syngnathus folletti		X	X
Familia Synbranchidae			
Synbranchus marmoratus	X		
Familia Scorpaenidae			
Helicolenus lahillei			X
Familia Congiopodidae			
Congiopodus peruvianus			X
Familia Triglidae			
Prionotus nudigula		X	X
Prionotus punctatus			X
Familia Polyprionidae			
Polyprion americanus			X
Familia Serranidae			
Acanthistius brasilianus			X
Dules auriga			X
Epinephelus guaza			X
Familia Pomatomidae			
Pomatomus saltatrix		X	X
Familia Carangidae			
Parona signata		X	X
Selene vomer			X
Trachurus picturatus			X
Trachinotus marginatus			X
Trachurus lathami		X	X
Vomer setapinnis			X
Familia Gerreidae			
Eucinostomus gula			X
Eucinostomus melanopterus		X	
Familia Sparidae			
Diplodus argenteus			X
Pagrus pagrus			X
Familia Haemulidae			
Boridia grossidens			X
Familia Sciaenidae			
Cynoscion guatucupa			X
Cynoscion striatus			X
Macrodon ancylodon	X		X
Menticirrhus americanus		X	X
Micropogonias furnieri			X
Pachyurus bonariensis	X		
Paralonchurus brasiliensis	X	X	X
Plagioscion ternetzi	X		
Pogonias cromis		X	X
Umbrina canosai			X
Familia Mullidae			
Mullus argentinae			X
Familia Cheilodactylidae			
Cheilodactylus bergi			X
Familia Cichlidae			
Australoheros facetus	X		

Crenicichla lacustris	X		
Crenicichla lepidota	X		
Gymnogeophagus australis	X		
Gymnogeophagus gymnogenys	X		
Gymnogeophagus meridionalis	X		
Gymnogeophagus rhabdotus	X		
Familia Nototheniidae			
Patagonotothen ramsayi			X
Familia Pinguipedidae			
Pinguipes brasilanus			X
Pseudopercis semifasciata			X
Familia Percophidae			
Percophis brasiliensis			X
Familia Uranoscopidae			
Astroscopus sexspinosus			X
Familia Blenniidae			
Hypleurochilus fissicornis			X
Familia Gobiidae			
Gobiosoma parri			X
Familia Sphyraenidae			
Sphyraena picudilla			X
Familia Gempylidae			
Thyrsitops lepidopodea			X
Familia Trichiuridae			
Trichiurus lepturus			X
Familia Scombridae			
Scomber japonicus			X
Familia Stromateidae			
Peprilus paru			X
Stromateus brasiliensis		X	X
Familia Paralichthyidae			
Etropus longimanus			X
Paralichthys isosceles			X
Paralichthys orbignyanus		X	X
Paralichthys patagonicus		X	X
Xystreuris rasile			X
Familia Pleuronectidae			
Oncopterus darwini		X	X
Familia Achiriidae			
Catathyridium jenynsii,	X		
Familia Cynoglossidae			
Symphurus jenynsii			
Symphurus plagiusa			
Familia Balistidae			
Balistes capriscus			X
Familia Tetraodontidae			
Lagocephalus laevigatus			X

Table 2. Oceanographic data (mean, standard deviation) of fish assemblages areas defined by multivariate analyses using biomass (t nm^{-2}) or abundance (thousands ind nm^{-2}). Z, total depth (m); ST, surface temperature (°C); BT, bottom temperature (°C); SS, surface salinity (SPU); BS, bottom salinity (SPU).

		Riverine	Estuarine	Shelf	Slope
Biomass	**Z**	7.88 ± 1.53	6.29 ± 2.69	28 ± 12.75	151.66 ± 107.51
	ST	20.55 ± 0.35	20 ± 0.99	18.41 ± 1.59	15.33 ± 0.99
	BT	20.46 ± 0.45	19.32 ± 0.803	14.88 ± 2.11	6.99 ± 2.28
	SS	0.08 ± 0.02	9.96 ± 8.66	26.85 ± 4.48	33.45 ± 0.3
	BS	0.08 ± 0.02	12.7 ± 8.93	31.61 ± 1.45	33.82 ± 0.25
		Riverine	**Estuarine**	**Shelf**	**Slope**
Abundance	**Z**	6.91 ± 2.33	7.75 ± 2.06	28 ± 12.75	151.66 ± 107.51
	ST	20.4 ± 0.54	19.99 ± 1.21	18.41 ± 1.59	15.33 ± 0.99
	BT	20.28 ± 0.56	18.96 ± 0.75	14.88 ± 2.11	6.99 ± 2.28
	SS	1.15 ± 2.34	14.43 ± 8.98	26.85 ± 4.48	33.45 ± 0.3
	BS	1.2 ± 2.44	19.07 ± 5.04	31.61 ± 1.45	33.82 ± 0.25

Table 3. Estimates of mitochondrial DNA polymorphism in different fish models. Variables and phylogenetic informative sites in the total data set; haplotype diversity and nucleotide diversity (Nei 1987).

Species	*Brevoortia aurea*	*Engraulis anchoita*	*Squatina guggenheim*
mitochondrial *Cyt-b* Gene (bp)	720	720	448
Variable Sites	199	119	295
Phylogenetic informative Sites	88	60	128
Number of Haplotypes	46	14	15
Haplotype Diversity (SD)	1.000 (0.005)	0.978 (0.003)	0.382 (0.078)
Nucleotide diversity (SD)	0.06 (0.015)	0.060 (0.030)	0.011 (0.003)

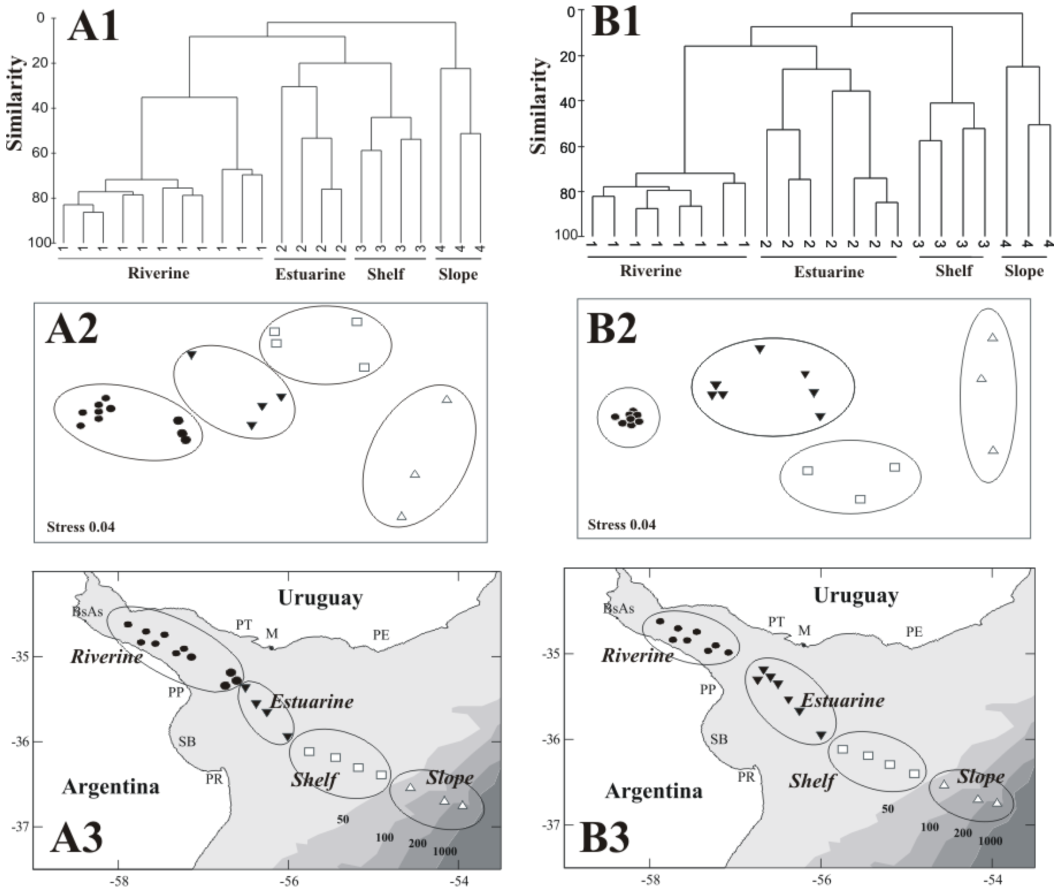

Figure. 1. Dendograms of the cluster analysis (1), nMDS diagrams (2) and location of the fish assemblages areas (3) defined for abundance (A) and biomass (B) analysis.

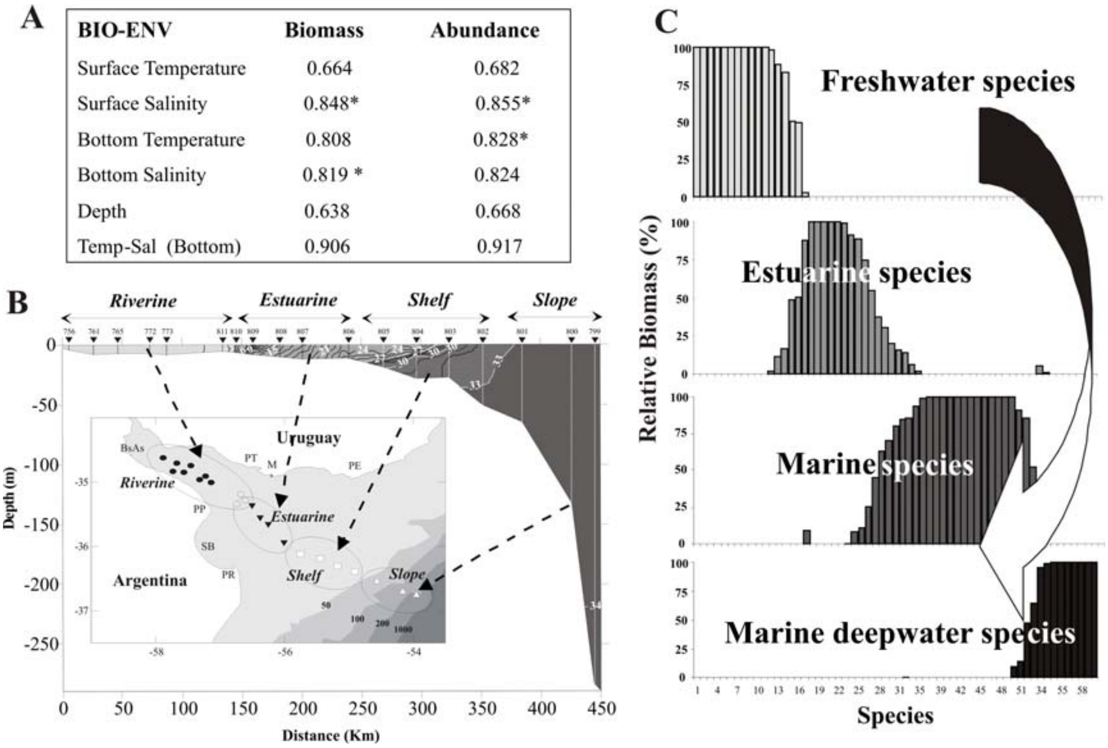

Figure. 2. A) Combination of the environmental variables yielding the best matches of biotic (species biomass or abundance, Bray Curtis similarity), and abiotic (Euclidean distance) similarity matrices, as measured by weighted Spearman correlation by means of BIO-ENV process. Z, depth (m); ST, surface temperature (ºC); BT, bottom temperature (ºC); SS, surface salinity; BS, bottom salinity. B) Location of the fish assemblage areas defined using biomass on the distribution of salinity along the sampling station, and their area of distribution. C) Relative biomass (%) of the species by fish assemblage area defined by multivariate analyses using biomass (t/nm^2). *(1) A. valenciennesi, (2) B. chauliodon, (3) C. carpio, (4) H. laplatae, (5) L. obtusidens, (6) P. bonariensis, (7) P. vetula, (8) P. maculatus, (9) P. lineatus, (10) P. granulosus, (11) N.barba, (12) R. dorbignyi, (13)*

P. albicans, (14) L. pati, (15) P. valenciennesi, (16) L. grossidens, (17) M. furnieri, (18) A. marinii, (19) B. aurea, (20) C. orbignyanus, (21) C. guatucupa, (22) P. brasiliensis, (23) M. ancylodon, (24) P. punctatus, (25) P. signata, (26) S. bonapartii, (27) P. patagonicus, (28) M. goodei, (29) T. lepturus, (30) M. schmitti, (31) R. agassizi, (32) S. guggenheim, (33) S. brasiliensis, (34) T. lathami, (35) A. brasilianus, (36) A.castelnaui, (37) D auriga, (38) G. galeus, (39) M. argentinae, (40) Myliobatis sp., (41) P. pagrus, (42) P. brasiliensis, (43) P. nudigula, (44) P. semifasciata, (45) S. megalops, (46) T. lepidopodea, (47) Z. brevirostris, (48) D. tschudii, (49) X. rasile, (50) C. bergi, (51) M. hubbsi, (52) U.brasiliensis, (53) B. albesens, (54) C. c. marinii, (55) G. blacodes, (56) H. lahillei, (57) M. magallanicus, (58) P. ramsayi, (59) S. acanthias, (60) S. mitsukurii.

Figure 3. Phylogenetic reconstruction using neighbour joining tree based on HKY85 model of molecular substitution. This model was obtained using hierarchical likelihood ratio tests (Huelsenbeck & Crandall, 1997) implemented in MODELTEST 3.06 (Posada & Crandall, 1998). Sixty individuals sampled belong to four collecting sites: Inner Shelf 35ºS 53ºW; Inner Shelf 36ºS 54ºW; Outer Shelf; Outer Río de la Plata. Numbers above branches represent 50% bootstrap supports.

Figure 4 Phylogenetic reconstruction using neighbour joining tree based on GTR model of molecular substitution. This model was obtained using hierarchical likelihood ratio tests (Huelsenbeck & Crandall, 1997) implemented in MODELTEST 3.06 (Posada & Crandall, 1998). Seventy individuals sampled belong to three collecting sites: Atlantic Ocean coast; Outer Shelf; Outer Río de la Plata. Numbers above branches represent 50% bootstrap supports.